```
(FILE 'HOME' ENTERED AT 14:15:14 ON 08 JUN 2006)

      FILE 'REGISTRY' ENTERED AT 14:15:23 ON 08 JUN 2006
L1         14340 SEA PLU=ON   CCCGGCGCGCT|AGCGCGCCGGG/SQSN


      FILE 'CAPLUS' ENTERED AT 14:16:45 ON 08 JUN 2006
L2              QUE PLU=ON   L1
L3          431 SEA PLU=ON   L2 AND (VECTOR)
L4           46 SEA PLU=ON   L3 AND PY<2000
                D TI 1-46
                D IBIB AB 25
                D HIT RN 25
L5            1 SEA PLU=ON   L1 AND  140780-42-3/RN
                D ALL


      FILE 'REGISTRY' ENTERED AT 14:19:24 ON 08 JUN 2006
L6            1 SEA PLU=ON   L1 AND  140780-42-3/RN
                D KWIC
                D ALL
```

## O'Bryen, Barbara

___

**From:**     Switzer, Juliet
**Sent:**     Monday, May 08, 2006 10:56 AM
**To:**       O'Bryen, Barbara
**Subject:** RE: problem with sequence search request

Regarding the last part- I figured as that was the problem and I'm sorry I even said anything since I know that you always diligently do your work (which is often my work). Is that a little bit of a drag that a contractor is doing all of the "easy" searches? My last one she searched MORE databases than I asked for- is it worth mentioning this to anyone (like her or Mary)? She mentioned when she wrote me to tell me my results are available in SCORE that there's a backlog- this would be helped by not over searching, but I don't want to be a pain. I'm just glad when I get my searches back.

Regarding parts 3 and 4, I think it would be fine to do them as you suggest- I think between that and the score/length search I should be able to determine what I need to know. Can you give me extra hits and alignments, thought? (maybe 500/100?). Thank you very much for looking into this and helping me figure it out. I really appreciate it when you pick up my searches!

talk to you soon- hope you are enjoying the spring.

Juliet

> -----Original Message-----
> **From:** O'Bryen, Barbara
> **Sent:** Monday, May 08, 2006 10:36 AM
> **To:** Switzer, Juliet
> **Subject:** RE: problem with sequence search request
>
> Juliet,
> I just rechecked the running times on this search, & the total is only 23 hrs. I'm not sure how I got the 41 hrs. Maybe I put in the wrong fragments for Seq 1. Parts 3&4 are pretty redundant, though. Would it be ok for me to replace nt 3336 with an "n" & run the seach with the DX matrix? That would allow the N in the query to match any thing in the database, & the match would be marked with a colon ( : ), which makes it easier to find if you're just eyeballing the alignment. Deleting one base is a little silly, because the search algorithm allows for gaps, mismatches, insertions, & deletions. I can't imagine that the results for parts 3 & 4 would be any different. Cutting out one of them will bring the total number of run time hours down to 19, which would be perfect. What do you think?
>
> As far as turnaround times go, if you have just a straightforward search, it should be processed fairly quickly. (We have a contractor who does nothing but the simple seq searches. She's pretty diligent, but unfortunately also has 'other duties as assigned'.) For non-straightforward requests (especially one with five (!) score over length searches), I'm afraid a long lag between request & pick up isn't unusual.

Barb

-----Original Message-----
**From:** Switzer, Juliet
**Sent:** Friday, May 05, 2006 9:49 PM
**To:** O'Bryen, Barbara
**Subject:** RE: problem with sequence search request

Barb,
No problem about the form letter- is there a particular part of the search that is too long- can you give me any guidance about what you can do from what I requested?  This is for a case I inherited from someone who left the office.  When I get in Monday I'll take the search to someone to try to come up with a better solution- but any input from you would be helpful.  Silly me, I thought I'd be getting these results soon- is 10 days from request to pick up the typical wait time now?

Thanks, Barb.  See you soon, Juliet

-----Original Message-----
**From:** O'Bryen, Barbara
**Sent:** Fri 5/5/2006 12:12 PM
**To:** Switzer, Juliet
**Cc:**
**Subject:** problem with sequence search request

Hi Juliet,
Excuse the form letter, but this search is just too darn long!
Barb

You recently submitted the search request included below.
I'm now working on the search, but unfortunately the search as requested would take too long to process.

In order to make the most fair use of system resources, the following criteria have been developed for search requests:
1) no more than 10 nucleic acid sequences
2) no sequences >9,999 nt long
3) total search time must be <20 hrs

The search is projected to take ~41 hrs on our fastest machine, so this search cannot be processed.  This time estimate does not include the extensive post-processing required for score over length searches.

Please contact one of the examiners listed below, who may be able to help you reduce the size of your request, or can give special authorization to have the search run as is.

Scott Priebe
Jim Martinell
Mike Pak
Jeff Fredman

Please forward the changes or approval directly to me (**not** to the STIC-Biotech/ChemLib mailbox) since I have the request on my desk .

5/8/06

Thanks,
Barb
2-2518

-----Original Message-----
**From:** STIC-Biotech/ChemLib
**Sent:** Friday, May 05, 2006 12:08 PM
**To:** O'Bryen, Barbara
**Subject:** FW: sequence search request

-----Original Message-----
**From:** Switzer, Juliet
**Sent:** Monday, April 24, 2006 10:36 AM
**To:** STIC-Biotech/ChemLib
**Subject:** sequence search request

for 09/904968, please complete the following searches:

1. For each of seq id no 3, 4, 19, and 20, please do a score over length search, length minimum 10, length maximum the length of the sequence, score over length cut off of 70%.

2. For seq id no 1, nucleotides 3326-3346 with nucloetide 3336 deleted, please do a score over length search, length minimum 10, length maximum 20, score over length cut off of 70%.

3. Please search in all prior art nucleic acid databases seq id no 1 nucleotides 3300-3400 where nucleotide 3336 is deleted.

4. Please search in all prior art nucleic acid databases seq id no 1 nucleotides 3300-3400.

5. Please provide a search in US PATENT databases, including interference for seq di no 3, 4, 19, and 20.

THANKS,


Juliet Switzer
Art Unit 1634
phone: 571-272-0753
office: Remsen 2A61
mailbox: 2C70

5/8/06